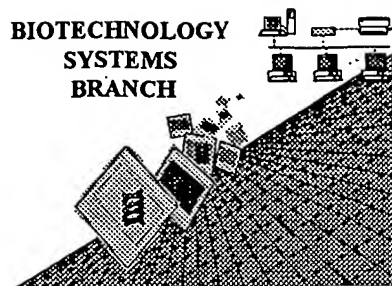


5630 #5



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,723
Source: P4/112
Date Processed by STIC: 1/14/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTEDSUGGESTED CORRECTION

SERIAL NUMBER: 10/009,723

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,723

DATE: 01/14/2002

TIME: 07:56:08

Does Not Comply
Corrected Diskette Needed

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
 5 <120> TITLE OF INVENTION: Diagnostic and therapeutic agents for the diseases related
 monocytes and
 6 macrophages
 8 <130> FILE REFERENCE: 11214WO1
 10 <140> CURRENT APPLICATION NUMBER: US/10/009,723
 11 <141> CURRENT FILING DATE: 2001-12-17
 13 <150> PRIOR APPLICATION NUMBER: H11-171709
 14 <151> PRIOR FILING DATE: 1999-06-17
 16 <160> NUMBER OF SEQ ID NOS: 92
 18 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

100 <210> SEQ ID NO: 3
 101 <211> LENGTH: 409
 102 <212> TYPE: DNA
 103 <213> ORGANISM: Mus musculus
 105 <220> FEATURE:
 106 <223> OTHER INFORMATION:
 108 <220> FEATURE:
 109 <221> NAME/KEY: CDS
 110 <222> LOCATION: (1)..(408)
 112 <400> SEQUENCE: 3
 113 atg gga ttc agc agg atc ttt ctc ttc ctc ctg tca gtg act aca ggt 48
 114 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 W--> 115 -19 -15 -15 -10 -5 ← misaligned amino
 116 gtc cac tcc cag gct ttt cta cag cag tct ggg gct gag ctg gtg agg 96
 117 Val His Ser Gln Ala Phe Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 W--> 118 -1 1 5 10 same error
 119 cct ggg gcc tca gtg aag atg tcc tgc aag gct tct ggc tac aca ttt 144
 120 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 W--> 121 15 20 25 same
 122 atc aat tae aat atg cac tgg gta aag cag aca cct aga cag ggc ctg 192
 123 Ile Asn Tyr Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu
 W--> 124 30 35 40 45 same
 125 gaa tgg att gga gct att ttt cca gga aat ggt ttt act tcc tac aat 240
 126 Glu Trp Ile Gly Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn
 W--> 127 50 55 60 same
 128 cag aag ttc aag ggc aag gcc aca ctg act gta gac aaa tcc tcc agc 288
 129 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
 W--> 130 65 70 75 same
 131 aca gtc tac atg cag ctc cgc agc ctg aca tct gaa gac tct gcg gtc 336
 E--> 132 thr val tyr met gln leu arg ser leu thr ser glu asp ser ala val 80
 E--> 133 85 90 misaligned
 E--> 134 tat ttc tgt gca aga gat ggt gac tat tac ttt gac tac tgg ggc caa 384
 135 Tyr Phe Cys Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln

(global error)

misaligned amino
acid
numbers(see item 3
on Error
summary
sheet)insert a hard
return

initial letter of amino acid is always in upper-case letter

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/009,723

DATE: 01/14/2002
 TIME: 07:56:07

Input Set : A:\ES.txt
 Output Set: N:\CRF3\01142002\J009723.raw

W--> 136 95 100 105 *misaligned*
 E--> 137 ggc acc act ctc aca gtc tcc tca g 409
 138 Gly Thr Thr Leu Thr Val Ser Ser
 E--> 139 110 115 117 *misaligned*
 179 <210> SEQ ID NO: 5
 180 <211> LENGTH: 5
 181 <212> TYPE: PRT
 182 <213> ORGANISM: Mus musculus
 184 <220> FEATURE:
 185 <223> OTHER INFORMATION:
 187 <400> SEQUENCE: 5
 188 Ser Asn Tyr Ile Ser
 E--> 189 1 5 5 *misaligned*
 191 <210> SEQ ID NO: 6
 192 <211> LENGTH: 17
 193 <212> TYPE: PRT
 194 <213> ORGANISM: Mus musculus
 196 <220> FEATURE:
 197 <223> OTHER INFORMATION:
 199 <400> SEQUENCE: 6
 200 Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn Gln Lys Phe Thr
 E--> 201 1 5 10 15
 202 Ala
 203 17
 205 <210> SEQ ID NO: 7
 206 <211> LENGTH: 10
 207 <212> TYPE: PRT
 208 <213> ORGANISM: Mus musculus
 210 <220> FEATURE:
 211 <223> OTHER INFORMATION:
 213 <400> SEQUENCE: 7
 214 His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr
 E--> 215 1 5 10
 217 <210> SEQ ID NO: 8
 218 <211> LENGTH: 10
 219 <212> TYPE: PRT
 220 <213> ORGANISM: Mus musculus
 222 <220> FEATURE:
 223 <223> OTHER INFORMATION:
 225 <400> SEQUENCE: 8
 226 Ser Ala Ser Ser Ser Val Ser Tyr Met His
 E--> 227 1 5 10
 229 <210> SEQ ID NO: 9
 230 <211> LENGTH: 7
 231 <212> TYPE: PRT
 232 <213> ORGANISM: Mus musculus
 234 <220> FEATURE:
 235 <223> OTHER INFORMATION:
 237 <400> SEQUENCE: 9

*Per 1.822 of Sequence
 Rules, number the
 amino acids under
 every 5 amino
 acids
 (global env)*

same

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/009,723

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

238 Asp Thr Ser Lys Leu Pro Ser
 E--> 239 1 5 7 → number added after under every 5
 241 <210> SEQ ID NO: 10
 242 <211> LENGTH: 9
 243 <212> TYPE: PRT
 244 <213> ORGANISM: Mus musculus
 246 <220> FEATURE:
 247 <223> OTHER INFORMATION:
 249 <400> SEQUENCE: 10
 250 Gln Gln Trp Ser Ser Asn Pro Pro Thr
 E--> 251 1 5 9
 253 <210> SEQ ID NO: 11
 254 <211> LENGTH: 5
 255 <212> TYPE: PRT
 256 <213> ORGANISM: Mus musculus
 258 <220> FEATURE:
 259 <223> OTHER INFORMATION:
 261 <400> SEQUENCE: 11
 262 Asn Tyr Asn Met His
 E--> 263 1 5
 265 <210> SEQ ID NO: 12
 266 <211> LENGTH: 17
 267 <212> TYPE: PRT
 268 <213> ORGANISM: Mus musculus
 270 <220> FEATURE:
 271 <223> OTHER INFORMATION:
 273 <400> SEQUENCE: 12
 274 Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn Gln Lys Phe Lys
 E--> 275 1 5 10 15
 276 Gly
 277 17
 279 <210> SEQ ID NO: 13
 280 <211> LENGTH: 8
 281 <212> TYPE: PRT
 282 <213> ORGANISM: Mus musculus
 284 <220> FEATURE:
 285 <223> OTHER INFORMATION:
 287 <400> SEQUENCE: 13
 288 Asp Gly Asp Tyr Tyr Phe Asp Tyr
 E--> 289 1 5 8
 291 <210> SEQ ID NO: 14
 292 <211> LENGTH: 10
 293 <212> TYPE: PRT
 294 <213> ORGANISM: Mus musculus
 296 <220> FEATURE:
 297 <223> OTHER INFORMATION:
 299 <400> SEQUENCE: 14
 300 Ser Ala Ser Ser Ser Val Ser Tyr Met His
 E--> 301 1 5 10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,723

DATE: 01/14/2002

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

```

303 <210> SEQ ID NO: 15
304 <211> LENGTH: 7
305 <212> TYPE: PRT
306 <213> ORGANISM: Mus musculus
308 <220> FEATURE:
309 <223> OTHER INFORMATION:
311 <400> SEQUENCE: 15
312 Arg Thr Ser Asn Leu Ala Ser
E--> 313 1 5 7 same
315 <210> SEQ ID NO: 16
316 <211> LENGTH: 7
317 <212> TYPE: PRT
318 <213> ORGANISM: Mus musculus
320 <220> FEATURE:
321 <223> OTHER INFORMATION:
323 <400> SEQUENCE: 16
324 His Gln Trp Ser Met Tyr Thr
E--> 325 1 5 7 same
E--> 394 <210> SEQ ID NO: 22 23
395 <211> LENGTH: 33
396 <212> TYPE: DNA
397 <213> ORGANISM: Artificial Sequence
399 <220> FEATURE:
400 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
E--> 402 <400> SEQUENCE: 23
403 cgttcggagg ggggaccaag ctggaaataa aac 33
E--> 405 <210> SEQ ID NO: 24 ignore - this is due to above error
488 <210> SEQ ID NO: 31
489 <211> LENGTH: 421 415 (p.5)
490 <212> TYPE: DNA
491 <213> ORGANISM: Artificial Sequence
493 <220> FEATURE:
494 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
496 <220> FEATURE:
497 <221> NAME/KEY: CDS
498 <222> LOCATION: (1)..(420)
500 <400> SEQUENCE: 31
501 atg gaa tgg aac tgg gtc gtt ctc ttc ctc ctg tca tta act gca ggt 48
502 Met Glu Trp Asn Trp Val Val Leu Phe Leu Leu Ser Leu Thr Ala Gly
W--> 503 -19 -15 -10 -5
504 gtc tat gcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag 96
505 Val Tyr Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
W--> 506 -1 1 5 10
507 cct ggc gcc tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc 144
508 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
W--> 509 15 20 25
510 agc agt aac tat ata agt tgg gtg cga cag gcc cct gga caa ggg ctt 192
511 Ser Ser Asn Tyr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
W--> 512 30 35 40 45

```

*misaligned
hos.*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,723

DATE: 01/14/2002

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

```

513 gag tgg atg gga tgg att tat gct gga act ggt gat gcc agc tat aat 240
514 Glu Trp Met Gly Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn
W--> 515      50      55      60
516 cag aag ttc aca gcc aga gtc acc att acc gtc gac aca tcc acg agc 288
517 Gln Lys Phe Thr Ala Arg Val Thr Ile Thr Val Asp Thr Ser Thr Ser
W--> 518      65      70      75
519 aca gcc tac atg gag ctg age age ctg aga tct gag gac acg gcc gtg 336
520 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
W--> 521      80      85      90
522 tat tac tgt gag aga cac ggg ggg gac ggc tac tgg ttt gct tac tgg 384
523 Tyr Tyr Cys Ala Arg His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr Trp
W--> 524      95      100      105
525 ggc cag gga acc ctg gtc acc gtc tcc tca g
526 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
E--> 527 110      115
642 <210> SEQ ID NO: 39
643 <211> LENGTH: 87
644 <212> TYPE: DNA
645 <213> ORGANISM: Artificial Sequence
647 <220> FEATURE:
648 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
650 <400> SEQUENCE: 39
W--> 651 caggaaacag ctatgacgaa ttccaccatg gattttcaag tgcagatttt cagcttcctg 60ctaatacagtg
E--> 652 cctcagtcac aatatcc
654 <210> SEQ ID NO: 40
655 <211> LENGTH: 93
656 <212> TYPE: DNA
657 <213> ORGANISM: Artificial Sequence
659 <220> FEATURE:
660 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
662 <400> SEQUENCE: 40aagtgatggt gactctgtct cctacagatg cagacaggga ggaatggagac tgggtcatct
(60) see item 1 on Envs Summary sheet ↑ insert a hard return
E--> 663 ggatatctcc tetggatatt atgactgagg cac
974 <210> SEQ ID NO: 63
975 <211> LENGTH: (8) 85 shown
976 <212> TYPE: DNA
977 <213> ORGANISM: Artificial Sequence
979 <220> FEATURE:
980 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
982 <400> SEQUENCE: 63
983 agacagagtc accatcaactt gtagtgccag ctcgagtgtgta agttacatgc actggtatca 60
E--> 984 gcagaaacca gggaaagccc ctaag
1282 <210> SEQ ID NO: 82
1283 <211> LENGTH: 138
1284 <212> TYPE: PRT
1285 <213> ORGANISM: Mus musculus
1287 <220> FEATURE:
1288 <223> OTHER INFORMATION:
1290 <400> SEQUENCE: 82
1291 Met Glu Trp Asn Trp Val Val Leu Phe Leu Leu Ser Leu Thr Ala Gly

```

415

insert hard return

87

93

85 ←

P-6

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,723

DATE: 01/14/2002

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

```

1292 -19          -15          -10          -5
1293 Val Tyr Ala Gln Gly Gln Met Gln Gln Ser Gly Ala Glu Leu Val Lys
E--> 1294  -1  1      5      10
1295 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Pro Ser Gly Phe Thr Phe
E--> 1296  15      20      25
1297 Ser Ser Asn Tyr Ile Ser Trp Leu Lys Gln Lys Pro Gly Gln Ser Leu
E--> 1298  30      35      40      45
1299 Glu Trp Ile Ala Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn
E--> 1300  50      55      60
1301 Gln Lys Phe Thr Ala Lys Ala His Val Thr Val Asp Thr Ser Ser Ser
E--> 1302  65      70      75
1303 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Thr Glu Asp Ser Ala Ile
E--> 1304  80      85      90
1305 Tyr Tyr Cys Ala Arg His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr Trp
E--> 1306  95      100     105
1307 Gly Gln Gly Thr Leu Val Thr Val Ser Ala
E--> 1308 110     115     119
1310 <210> SEQ ID NO: 83
1311 <211> LENGTH: 128
1312 <212> TYPE: PRT
1313 <213> ORGANISM: Mus musculus
1315 <220> FEATURE:
1316 <223> OTHER INFORMATION:
1318 <400> SEQUENCE: 83
1319 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
E--> 1320 -22  -20      -15      -10
1321 Val Ile Ile Ser Arg Gly Gln Leu Val Leu Thr Gln Ser Pro Ala Ile
E--> 1322  -5      -1  1      5      10
1323 Met Ser Ala Ser Gln Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
E--> 1324  15      20      25
1325 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
E--> 1326  30      35      40
1327 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Pro Ser Gly Val Pro
E--> 1328  45      50      55
1329 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
E--> 1330  60      65      70
1331 Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
E--> 1332  75      80      85      90
1333 Ser Ser Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
E--> 1334  95      100     105  106
1336 <210> SEQ ID NO: 84
1337 <211> LENGTH: 136
1338 <212> TYPE: PRT
1339 <213> ORGANISM: Mus musculus
1341 <220> FEATURE:
1342 <223> OTHER INFORMATION:
1344 <400> SEQUENCE: 84
1345 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
E--> 1346 -19      -15      -10      -5

```

*misaligned
nos.*

*same
error*

same

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/1Q/009,723

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

1347 Val His Ser Gln Ala Phe Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 E--> 1348 -1 1 5 10
 1349 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 E--> 1350 15 20 25
 1351 Ile Asn Tyr Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu
 E--> 1352 30 35 40 45
 1353 Glu Trp Ile Gly Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn
 E--> 1354 50 55 60
 1355 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
 E--> 1356 65 70 75
 1357 Thr Val Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 E--> 1358 80 85 90
 1359 Tyr Phe Cys Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln
 E--> 1360 95 100 105
 1361 Gly Thr Thr Leu Thr Val Ser Ser
 E--> 1362 110 115 (117)
 1364 <210> SEQ ID NO: 85
 1365 <211> LENGTH: 126
 1366 <212> TYPE: PRT
 1367 <213> ORGANISM: Mus musculus
 1369 <220> FEATURE:
 1370 <223> OTHER INFORMATION:
 1372 <400> SEQUENCE: 85
 1373 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 E--> 1374 -22 -20 -15 -10
 1375 Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
 E--> 1376 -5 -1 1 5 10
 1377 Met Ser Ala Ser Leu Gly Glu Glu Ile Thr Leu Thr Cys Ser Ala Ser
 E--> 1378 15 20 25
 1379 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
 E--> 1380 30 35 40
 1381 Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro
 E--> 1382 45 50 55
 1383 Phe Arg Phe Ser Gly Ser Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile
 E--> 1384 60 65 70
 1385 Ser Ser Val Glu Ala Glu Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp
 E--> 1386 75 80 85 90
 1387 Ser Met Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 E--> 1388 95 100
 1390 <210> SEQ ID NO: 86
 1391 <211> LENGTH: 140
 1392 <212> TYPE: PRT
 1393 <213> ORGANISM: Artificial Sequence
 1395 <220> FEATURE:
 1396 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
 1398 <400> SEQUENCE: 86
 1399 Met Glu Trp Asn Trp Val Val Leu Phe Leu Leu Ser Leu Thr Ala Gly
 E--> 1400 -19 -15 -10 -5
 1401 Val Tyr Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

*same**same*

(104) number the amino acids under
 every 5 amino
 acids

same

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/009,723

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

```

E--> 1402      -1  1      5      10
      1403 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
E--> 1404      15      20      25
      1405 Ser Ser Asn Tyr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
E--> 1406      30      35      40      45
      1407 Glu Trp Met Gly Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn
E--> 1408      50      55      60
      1409 Gln Lys Phe Thr Ala Arg Val Thr Ile Thr Val Asp Thr Ser Thr Ser
E--> 1410      65      70      75
      1411 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
E--> 1412      80      85      90
      1413 Tyr Tyr Cys Ala Arg His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr Trp
E--> 1414      95     100     105
      1415 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
E--> 1416 110     115     119
      1418 <210> SEQ ID NO: 87
      1419 <211> LENGTH: 136
      1420 <212> TYPE: PRT
      1421 <213> ORGANISM: Artificial Sequence
      1423 <220> FEATURE:
      1424 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
      1426 <400> SEQUENCE: 87
      1427 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
      1428 -19      -15      -10      -5
      1429 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
      1430      -1  1      5      10
      1431 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      1432      15      20      25
      1433 Ile Asn Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      1434      30      35      40      45
      1435 Glu Trp Met Gly Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn
      1436      50      55      60
      1437 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Lys Ser Thr Ser
      1438      65      70      75
      1439 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
      1440      80      85      90
      1441 Tyr Tyr Cys Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln
E--> 1442 100     105
      1443 Gly Thr Leu Val Thr Val Ser Ser
E--> 1444 110     115     117
      1446 <210> SEQ ID NO: 88
      1447 <211> LENGTH: 128
      1448 <212> TYPE: PRT
      1449 <213> ORGANISM: Artificial Sequence
      1451 <220> FEATURE:
      1452 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
      1454 <400> SEQUENCE: 88
      1455 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
E--> 1456 -22     -20      -15      -10

```

*same**insert
hard
return**misaligned nos.*

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/009,723

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

```

1457 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
E--> 1458      -5      -1 1      5      10
1459 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
E--> 1460      15      20      25
1461 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
E--> 1462      30      35      40
1463 Pro Lys Leu Leu Ile Tyr Asp Thr Ser Lys Leu Pro Ser Gly Val Pro
E--> 1464      45      50      55
1465 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
E--> 1466      60      65      70
1467 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
E--> 1468      75      80      85      90
1469 Ser Ser Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
E--> 1470      95      100      105 (106)
1498 <210> SEQ ID NO: 90
1499 <211> LENGTH: 126
1500 <212> TYPE: PRT
1501 <213> ORGANISM: Artificial Sequence
1503 <220> FEATURE:
1504 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
1506 <400> SEQUENCE: 90
1507 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1508 -22      -20      -15      -10
1509 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
1510      -5      -1 1      5      10
1511 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
1512      15      20      25
1513 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
E--> 1514      30      35      40 Pro Lys Leu Leu Ile Tyr
E--> 1515 Arg Thr Ser Asn Leu Ala Ser Gly Val Pro
E--> 1516      45      50      55
1517 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
E--> 1518      60      65      70
1519 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Trp
E--> 1520      75      80      85      90
1521 Ser Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
E--> 1522      95      100      (104)
1552 <210> SEQ ID NO: 92
1553 <211> LENGTH: 126
1554 <212> TYPE: PRT
1555 <213> ORGANISM: Artificial Sequence
1557 <220> FEATURE:
1558 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
1560 <400> SEQUENCE: 92
1561 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1562 -22      -20      -15      -10
1563 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
1564      -5      -1 1      5      10
1565 Leu Ser Ala Ser Val Gly Glu Glu Val Thr Ile Thr Cys Ser Ala Ser

```

*misaligned
nos,*

*delete - number the amino acids
under every 5 amino
acids*

*40 Pro Lys Leu Leu Ile Tyr
Insert hard return*

(104) delete

p. 10

DATE: 01/14/2002

TIME: 07:56:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

	1566				15				20				25				
	1567	Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala
	1568				30					35					40		
	1569	Pro	Lys	Leu	Leu	Ile	Tyr	Arg	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
	1570			45					50					55			
	1571	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Phe	Tyr	Thr	Leu	Thr	Ile
E-->	1572		60				65					70	70				
	1573	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Trp
	1574	75				80						85					90
	1575	Ser	Met	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys		
	1576				95						100				104		

← fix this

104
delete

see next page for more error

10/009,723

11

insert a hard return
<210> 52
<211> 379<212> DNA
<213> Artificial Sequence

same error in Seq. 78

PST

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,723

DATE: 01/14/2002

TIME: 07:56:08

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:132 M:254 E: No. of Bases conflict, LENGTH:Input:80 Counted:384 SEQ:3
 L:132 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
 L:132 M:112 C: (48) String data converted to lower case,
 M:254 Repeated in SeqNo=3
 L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:139 M:252 E: No. of Seq. differs, <211>LENGTH:Input:409 Found:457 SEQ:3
 L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
 L:201 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
 L:215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
 L:227 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
 L:239 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
 L:251 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
 L:263 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11

VERIFICATION SUMMARY

DATE: 01/14/2002

PATENT APPLICATION: US/10/009,723

TIME: 07:56:08

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

L:275 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:289 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:313 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
L:325 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:394 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:22
L:402 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:23
L:405 M:214 E: (33) Seq.# missing, SEQ ID NO:23
L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:521 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:527 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:527 M:252 E: No. of Seq. differs, <211>LENGTH:Input:421 Found:415 SEQ:31
L:651 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:652 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:39
L:652 M:254 E: No. of Bases conflict, LENGTH:Input:87 Counted:17 SEQ:39
L:652 M:252 E: No. of Seq. differs, <211>LENGTH:Input:87 Found:17 SEQ:39
L:663 M:254 E: No. of Bases conflict, LENGTH:Input:93 Counted:33 SEQ:40
L:663 M:252 E: No. of Seq. differs, <211>LENGTH:Input:93 Found:33 SEQ:40
L:728 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:731 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:734 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:737 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:743 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:746 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:835 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:904 M:112 C: (48) String data converted to lower case,
L:984 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:85 SEQ:63
L:1216 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:1294 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:82
M:332 Repeated in SeqNo=82
L:1320 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:83
M:332 Repeated in SeqNo=83
L:1346 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:84
M:332 Repeated in SeqNo=84
L:1374 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:85
M:332 Repeated in SeqNo=85
L:1400 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:86
M:332 Repeated in SeqNo=86
L:1416 M:252 E: No. of Seq. differs, <211>LENGTH:Input:140 Found:138 SEQ:86
L:1442 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:87
M:332 Repeated in SeqNo=87
L:1444 M:252 E: No. of Seq. differs, <211>LENGTH:Input:136 Found:120 SEQ:87

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,723

DATE: 01/14/2002

TIME: 07:56:08

Input Set : A:\ES.txt

Output Set: N:\CRF3\01142002\J009723.raw

L:1456 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:88
M:332 Repeated in SeqNo=88
L:1514 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:90
L:1514 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=90
L:1522 M:252 E: No. of Seq. differs, <211>LENGTH:Input:126 Found:125 SEQ:90
L:1572 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:92